RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: *10/500,841*
Source: *PCT*
Date Processed by STIC: *7/15/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
   Room 1B03, Arlington, VA 22202

Revised 05/17/04

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,841

DATE: 07/15/2004

TIME: 10:17:00

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\07152004\J500841.raw**

```
      3  <110>  APPLICANT: SUNTORY LIMITED
      5  <120>  TITLE OF INVENTION: Glycosyltransferase GnT-V having neovascularization action
      7  <130>  FILE REFERENCE: DS07F927
C-->  9  <140>  CURRENT APPLICATION NUMBER: US/10/500,841
C-->  9  <141>  CURRENT FILING DATE: 2004-07-07
      9  <150>  PRIOR APPLICATION NUMBER: PCT/JP02/13879
     10  <151>  PRIOR FILING DATE: 2002-12-27
     12  <160>  NUMBER OF SEQ ID NOS: 13
```
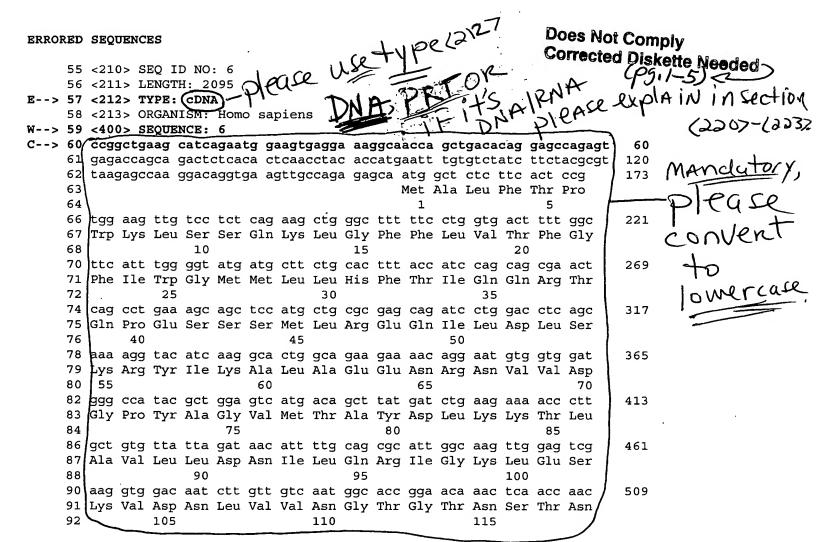
ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed →
(pg. 1-5)

— please use type (2127
DNA>PRIOR
if it's DNA/RNA please explain in section (2207-(2237

```
     55  <210>  SEQ ID NO: 6
     56  <211>  LENGTH: 2095
E--> 57  <212>  TYPE: (cDNA) — please use type (212)
     58  <213>  ORGANISM: Homo sapiens
W--> 59  <400>  SEQUENCE: 6
```

Mandatory, please convert to lowercase

```
C--> 60  ccggctgaag catcagaatg gaagtgagga aaggcaacca gctgacacag gagccagagt    60
     61  gagaccagca gactctcaca ctcaacctac accatgaatt tgtgtctatc ttctacgcgt   120
     62  taagagccaa ggacaggtga agttgccaga gagca atg gct ctc ttc act ccg       173
     63                                          Met Ala Leu Phe Thr Pro
     64                                           1               5
     66  tgg aag ttg tcc tct cag aag ctg ggc ttt ttc ctg gtg act ttt ggc    221
     67  Trp Lys Leu Ser Ser Gln Lys Leu Gly Phe Phe Leu Val Thr Phe Gly
     68                  10                  15                  20
     70  ttc att tgg ggt atg atg ctt ctg cac ttt acc atc cag cag cga act    269
     71  Phe Ile Trp Gly Met Met Leu Leu His Phe Thr Ile Gln Gln Arg Thr
     72                  25                  30                  35
     74  cag cct gaa agc agc tcc atg ctg cgc gag cag atc ctg gac ctc agc    317
     75  Gln Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser
     76              40                  45                  50
     78  aaa agg tac atc aag gca ctg gca gaa gaa aac agg aat gtg gtg gat    365
     79  Lys Arg Tyr Ile Lys Ala Leu Ala Glu Glu Asn Arg Asn Val Val Asp
     80  55                  60                  65                  70
     82  ggg cca tac gct gga gtc atg aca gct tat gat ctg aag aaa acc ctt    413
     83  Gly Pro Tyr Ala Gly Val Met Thr Ala Tyr Asp Leu Lys Lys Thr Leu
     84                  75                  80                  85
     86  gct gtg tta tta gat aac att ttg cag cgc att ggc aag ttg gag tcg    461
     87  Ala Val Leu Leu Asp Asn Ile Leu Gln Arg Ile Gly Lys Leu Glu Ser
     88                  90                  95                 100
     90  aag gtg gac aat ctt gtt gtc aat ggc acc gga aca aac tca acc aac    509
     91  Lys Val Asp Asn Leu Val Val Asn Gly Thr Gly Thr Asn Ser Thr Asn
     92              105                 110                 115
```

Same error

```
 94 tcc act aca gct gtt ccc agc ttg gtt gca ctt gag aaa att aat gtg    557
 95 Ser Thr Thr Ala Val Pro Ser Leu Val Ala Leu Glu Lys Ile Asn Val
 96     120                 125                 130
 98 gca gat atc att aac gga gct caa gaa aaa tgt gta ttg cct cct atg    605
 99 Ala Asp Ile Ile Asn Gly Ala Gln Glu Lys Cys Val Leu Pro Pro Met
100 135                 140                 145                 150
102 gac ggc tac cct cac tgt gag gga aag atc aag tgg atg aaa gac atg    653
103 Asp Gly Tyr Pro His Cys Glu Gly Lys Ile Lys Trp Met Lys Asp Met
104                 155                 160                 165
106 tgg cgt tca gat ccc tgc tac gca gac tat gga gtg gat gga tcc acc    701
107 Trp Arg Ser Asp Pro Cys Tyr Ala Asp Tyr Gly Val Asp Gly Ser Thr
108                 170                 175                 180
110 tgc tct ttt ttt att tac ctc agt gag gtt gaa aat tgg tgt cct cat    749
111 Cys Ser Phe Phe Ile Tyr Leu Ser Glu Val Glu Asn Trp Cys Pro His
112             185                 190                 195
114 tta cct tgg aga gca aaa aat ccc tac gaa gaa gct gat cat aat tca    797
115 Leu Pro Trp Arg Ala Lys Asn Pro Tyr Glu Glu Ala Asp His Asn Ser
116     200                 205                 210
118 ttg gcg gaa att cgt aca gat ttt aat att ctc tac agt atg atg aaa    845
119 Leu Ala Glu Ile Arg Thr Asp Phe Asn Ile Leu Tyr Ser Met Met Lys
120 215                 220                 225                 230
122 aag cat gaa gaa ttc cgg tgg atg aga cta cgg atc cgg cga atg gct    893
123 Lys His Glu Glu Phe Arg Trp Met Arg Leu Arg Ile Arg Arg Met Ala
124                 235                 240                 245
126 gac gca tgg atc caa gca atc aag tcc ctg gca gaa aag cag aac ctt    941
127 Asp Ala Trp Ile Gln Ala Ile Lys Ser Leu Ala Glu Lys Gln Asn Leu
128                 250                 255                 260
130 gaa aag aga aag cgg aag aaa gtc ctc gtt cac ctg gga ctc ctg acc    989
131 Glu Lys Arg Lys Arg Lys Lys Val Leu Val His Leu Gly Leu Leu Thr
132             265                 270                 275
134 aag gaa tct gga ttt aag att gca gag aca gct ttc agt ggt ggc cct   1037
135 Lys Glu Ser Gly Phe Lys Ile Ala Glu Thr Ala Phe Ser Gly Gly Pro
136     280                 285                 290
138 ctt ggt gaa tta gtt caa tgg agt gat tta att aca tct ctg tac tta   1085
139 Leu Gly Glu Leu Val Gln Trp Ser Asp Leu Ile Thr Ser Leu Tyr Leu
140 295                 300                 305                 310
142 ctg ggc cat gac att agg att tca gct tca ctg gct gag ctc aag gaa   1133
143 Leu Gly His Asp Ile Arg Ile Ser Ala Ser Leu Ala Glu Leu Lys Glu
144                 315                 320                 325
146 atc atg aag aag gtt gta gga aac cga tct ggc tgc cca act gta gga   1181
147 Ile Met Lys Lys Val Val Gly Asn Arg Ser Gly Cys Pro Thr Val Gly
148                 330                 335                 340
150 gac aga att gtt gag ctc att tac att gat att gta gga ctt gct caa   1229
151 Asp Arg Ile Val Glu Leu Ile Tyr Ile Asp Ile Val Gly Leu Ala Gln
152             345                 350                 355
154 ttc aag aaa act ctt gga cca tcc tgg gtt cat tac cag tgc atg ctc   1277
155 Phe Lys Lys Thr Leu Gly Pro Ser Trp Val His Tyr Gln Cys Met Leu
156     360                 365                 370
158 cga gtc ctt gat tca ttt ggt act gaa ccc gaa ttt aat cat gca aat   1325
```

Same error

159	Arg Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn	
160	375 380 385 390	
162	tat gcc caa tcg aaa ggc cac aag acc cct tgg gga aaa tgg aat ctg	1373
163	Tyr Ala Gln Ser Lys Gly His Lys Thr Pro Trp Gly Lys Trp Asn Leu	
164	395 400 405	
166	aac cct cag cag ttt tat acc atg ttc cct cat acc cca gac aac agc	1421
167	Asn Pro Gln Gln Phe Tyr Thr Met Phe Pro His Thr Pro Asp Asn Ser	
168	410 415 420	
170	ttt ctg ggg ttt gtg gtt gag cag cac ctg aac tcc agt gat atc cac	1469
171	Phe Leu Gly Phe Val Val Glu Gln His Leu Asn Ser Ser Asp Ile His	
172	425 430 435	
174	cac att aat gaa atc aaa agg cag aac cag tcc ctt gtg tat ggc aaa	1517
175	His Ile Asn Glu Ile Lys Arg Gln Asn Gln Ser Leu Val Tyr Gly Lys	
176	440 445 450	
178	gtg gat agc ttc tgg aag aat aag aag atc tac ttg gac att att cac	1565
179	Val Asp Ser Phe Trp Lys Asn Lys Lys Ile Tyr Leu Asp Ile Ile His	
180	455 460 465 470	
182	aca tac atg gaa gtg cat gca act gtt tat ggc tcc agc aca aag aat	1613
183	Thr Tyr Met Glu Val His Ala Thr Val Tyr Gly Ser Ser Thr Lys Asn	
184	475 480 485	
186	att ccc agt tac gtg aaa aac cat ggt atc ctc agt gga cgg gac ctg	1661
187	Ile Pro Ser Tyr Val Lys Asn His Gly Ile Leu Ser Gly Arg Asp Leu	
188	490 495 500	
190	cag ttc ctt ctt cga gaa acc aag ttg ttt gtt gga ctt ggg ttc cct	1709
191	Gln Phe Leu Leu Arg Glu Thr Lys Leu Phe Val Gly Leu Gly Phe Pro	
192	505 510 515	
194	tac gag ggc cca gct ccc ctg gaa gct atc gca aat gga tgt gct ttt	1757
195	Tyr Glu Gly Pro Ala Pro Leu Glu Ala Ile Ala Asn Gly Cys Ala Phe	
196	520 525 530	
198	ctg aat ccc aag ttc aac cca ccc aaa agc agc aaa aac aca gac ttt	1805
199	Leu Asn Pro Lys Phe Asn Pro Pro Lys Ser Ser Lys Asn Thr Asp Phe	
200	535 540 545 550	
202	ttc att ggc aag cca act ctg aga gag ctg aca tcc cag cat cct tac	1853
203	Phe Ile Gly Lys Pro Thr Leu Arg Glu Leu Thr Ser Gln His Pro Tyr	
204	555 560 565	
206	gct gaa gtt ttc atc ggg cgg cca cat gtg tgg act gtt gac ctc aac	1901
207	Ala Glu Val Phe Ile Gly Arg Pro His Val Trp Thr Val Asp Leu Asn	
208	570 575 580	
210	aat cag gag gaa gta gag gat gca gtg aaa gca att tta aat cag aag	1949
211	Asn Gln Glu Glu Val Glu Asp Ala Val Lys Ala Ile Leu Asn Gln Lys	
212	585 590 595	
214	att gag cca tac atg cca tat gaa ttt acg tgc gag ggg atg cta cag	1997
215	Ile Glu Pro Tyr Met Pro Tyr Glu Phe Thr Cys Glu Gly Met Leu Gln	
216	600 605 610	
218	aga atc aat gct ttc att gaa aaa cag gac ttc tgc cat ggg caa gtg	2045
219	Arg Ile Asn Ala Phe Ile Glu Lys Gln Asp Phe Cys His Gly Gln Val	
220	615 620 625 630	
222	atg tgg cca ccc ctc agc gcc cta cag gtc aag ctt gct gag ccc ggg	2093
223	Met Trp Pro Pro Leu Ser Ala Leu Gln Val Lys Leu Ala Glu Pro Gly	

```
      224                   635                640                645
      226 cc
      236 <210> SEQ ID NO: 8                                              2095
      237 <211> LENGTH: 24
E--> 238 <212> TYPE: cDNA
      239 <213> ORGANISM: Artificial Sequence
W--> 240 <220> FEATURE:
      241 <223> OTHER INFORMATION:
W--> 242 <400> SEQUENCE: 8
C--> 243 gggagtgagg atgatgtagg gaag
      245 <210> SEQ ID NO: 9                                 24
      246 <211> LENGTH: 24
E--> 247 <212> TYPE: cDNA
      248 <213> ORGANISM: Artificial Sequence
W--> 249 <220> FEATURE:
      250 <223> OTHER INFORMATION:
W--> 251 <400> SEQUENCE: 9
C--> 252 atggggcaga ggaacttacg ttat
      262 <210> SEQ ID NO: 11                                24
      263 <211> LENGTH: 6
      264 <212> TYPE: PRT
      265 <213> ORGANISM: Homo sapiens
      266 <223> OTHER INFORMATION: KRKRKK peptide
      267 <400> SEQUENCE: 11
      268 Lys Arg Lys Arg Lys Lys
      269   1                   5
      271 <210> SEQ ID NO: 12
      272 <211> LENGTH: 6
      273 <212> TYPE: PRT
      274 <213> ORGANISM: Homo sapiens
      275 <223> OTHER INFORMATION: FSGGPL peptide
      276 <400> SEQUENCE: 12
      277 Phe Ser Gly Gly Pro Leu
      278   1                   5
```

Handwritten annotations:
- please use type (212), DNA) PRT or if DNA/RNA, please explain in section <220> - <223>.
- Mandatory.
- if <213> is Artificial/ unknown, please explain in section <220> - <223>.
- pls Use lowercase
- SAMe error
- SAMe error
- pls convert to lowercase
- pls insert <220>, whenever <221>, <222> or <223> is present.
- pls insert <220> whenever, <221>, <222> or <223> is present.
- OK (E)
- OK (E)

VERIFICATION SUMMARY DATE: 07/15/2004
PATENT APPLICATION: **US/10/500,841** TIME: 10:17:01

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\07152004\J500841.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:18 M:283 W: Missing Blank Line separator, <400> field identifier
L:26 M:283 W: Missing Blank Line separator, <400> field identifier
L:34 M:283 W: Missing Blank Line separator, <400> field identifier
L:43 M:283 W: Missing Blank Line separator, <400> field identifier
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:59 M:283 W: Missing Blank Line separator, <400> field identifier
L:60 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=6
L:232 M:283 W: Missing Blank Line separator, <400> field identifier
L:238 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:240 M:283 W: Missing Blank Line separator, <220> field identifier
L:242 M:283 W: Missing Blank Line separator, <400> field identifier
L:242 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:241
L:243 M:112 C: (48) String data converted to lower case
L:247 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:249 M:283 W: Missing Blank Line separator, <220> field identifier
L:251 M:283 W: Missing Blank Line separator, <400> field identifier
L:251 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:250
L:252 M:112 C: (48) String data converted to lower case,
L:258 M:283 W: Missing Blank Line separator, <400> field identifier
L:267 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:276 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12
L:276 M:283 W: Missing Blank Line separator, <400> field identifier
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
```

```
<210> 13
<211> 5
<212> PRT
<213> Homo sapiens
<400> 13
His Phe Thr Ile Gln
 1               5
```

1/10 delete